REMARKS

The office action of December 31, 2003 has been reviewed and its contents carefully noted. Reconsideration of this case, as amended, is requested. Claims 1-22 and 24-26 remain in this case, claims 2, 10 and 20 being amended by this response.

The Applicant's agent would like to thank the Examiner for a telephone interview on April 13, 2004. In the interview, many of the rejections were discussed. The Examiner and the Applicant's agent disagreed regarding the requirement for a deposit.

The Examiner also stated that the claims were not enabled because Applicant had not shown that GMPase, or any of the other genes claimed, can increase Vitamin C biosynthesis over the wild type plants. The Examiner stated that there was no utility for the complementation experiments, and that it was not the same as putting the gene into a wild type plant. Applicant's agent explained that the claims are enabled, as written, and that is all that is required. The Examiner disagreed.

The Examiner then interpreted the references she cited against us in support of her enablement rejection. She said her strongest argument was based on Gatzek, which showed that the second to last enzyme in the proposed pathway did not increase Vitamin C biosynthesis. She said that, since an enzyme in another pathway does increase Vitamin C biosynthesis (Agius), and an enzyme in the pathway in the present application does not, that indicates that no enzyme in our pathway increases Vitamin C biosynthesis. She then stated it was now Applicant's burden to prove otherwise. Her argument was that adding an enzyme (Gatzek's enzyme) from the pathway in the present application has no effect. Therefore, she concluded that, until we provide evidence to the contrary, she has shown that no enzymes from the pathway in the present application would have an effect.

Applicant's agent explained that the references merely show that one enzyme in the pathway in the present application (an enzyme which is not found in the current claims) did not increase Vitamin C biosynthesis. The reference is silent about what other enzyme in the pathway might be the rate limiting step, or how their results impact the other enzymes in the pathway.

Applicant's agent stressed that that the Examiner's conclusion is not warranted from the evidence, and is not supported by the patent law of enablement.

Examiner stated that Applicant could overcome her enablement rejections by transforming GMPase into a wild type plant and showing that its different from Gatzek, and depositing the gene in ATCC (plasmid, subclone, or BACT517). The details of the telephone interview are described further herein, as they relate to the specific rejections raised by the Examiner.

The numbered paragraphs below correspond to the numbered paragraphs in the Office Action.

Objections to the Claims

5. Claims 6-7, 13-14 and 20-21 were objected to for failing to further limit the subject matter of a previous claim. Applicant respectfully disagrees.

37 C.F.R 1.75(c) states that "one or more claims may be presented in dependent form, referring back to and further limiting another claim or claims in the same application." The Examiner states that increasing the levels of Vitamin C in a plant and increasing the resistance to environmental stress "would be inherent features of the plants of parent claims 1 and 9 and an inherent result of the method of parent claims 16." (present office action dated December 31, 2003, page 2, lines 17-19). Even if these were inherent features of the plants and/or method, which the Applicant does not concede or deny, it is irrelevant to the question of whether claims 6-7, 13-14 and 20-21 further limit claims 1, 9, and 16, respectively. These claims add limitations, which clearly are not found in the parent claims.

M.P.E.P. 608.01(n) discusses 35 U.S.C. 112, fourth paragraph (which requires that a dependent claim "specify a further limitation of the subject matter claimed") and states that "a dependent claim does not lack compliance with 35 U.S.C. 112, fourth paragraph simply because there is a question as to (1) the significance of the further limitation added by the dependent claim, or (2) whether the further limitation in fact changes the scope of the dependent claim from that of the claim from which it depends. The test for a proper dependent claim under the fourth

paragraph of 35 U.S.C. 112 is whether the dependent claim includes every limitation of the claim from which it depends. The test is not one of whether the claims differ in scope."

Since claims 6-7, 13-14 and 20-21 clearly add limitations not in the parent claims upon which they depend, Applicant respectfully requests reconsideration and withdrawal of the objection.

Rejections under 35 U.S.C. §112

6. Claims 1-22 and 24-26 were rejected under 35 U.S.C. § 112, first paragraph, as lacking enablement. Applicant respectfully disagrees with the rejection, and believes that the claims, as amended, are enabled by the specification.

The test for enablement is whether the disclosure, when originally filed, contained sufficient information regarding the subject matter of the claims as to enable those of ordinary skill in the pertinent art to make and use the invention. The standard is whether the experimentation necessary to practice the invention is undue or unreasonable. In re Wands, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). See also U.S. v. Telectronics, Inc., 857 F.2d 778, 785, 8 USPQ2d 1217, 1223 (Fed. Cir. 1988) ("The test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation.") (emphasis added).

It is further noted that satisfaction of the enablement requirement is not precluded by the necessity of some experimentation, such as routine experimentation. The key word here is "undue" not "experimentation". In re Angstadt, 190 USPQ 214 (CCPA 1976). The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. In re Certain Limited-Charge Cell Culture Microcarriers, 221 USPQ 1165, 1174 (Int'l Trade Comm'n 1983), aff'd. sub nom., Massachusetts Institute of Technology v. A.B. Fortia, 774 F.2d 1104, 227 USPQ 428 (Fed. Cir. 1985). See also In re Wands, 858 F.2d at 737, 8 USPQ2d at 1404. Indeed, a considerable amount of experimentation is permissible if it is merely routine, or if the specification provides a reasonable amount of guidance to the direction in which the experimentation should proceed. In re Jackson, 217 USPQ 804 (Bd. App. 1982). Thus, the test of enablement is not whether any experimentation is necessary, but whether, if

experimentation is necessary, it is undue. In re Angstadt, 537 F.2d 498, 504, 190 USPQ 214, 219 (CCPA 1976).

Further, the specification need not explicitly teach those in the art to make and use the invention; the requirement is satisfied if, given what they already know, the specification teaches those in the art enough that they can make and use the invention without "undue experimentation." Genentech, Inc. v. Novo Nordisk, A/S, 108 F.3d 1361, 1365, 42 USPQ2d 1001, 1004 (Fed. Cir. 1997); In re Vaeck, 947 F.2d 488, 495, 20 USPQ2d 1438, 1444 (Fed. Cir. 1991). Indeed, a patent need not teach, and preferably omits, what is well known in the art. In re Buchner, 929 F.2d 660, 661, 18 USPQ2d 1331, 1332 (Fed. Cir. 1991); Hybritech, Inc. v. Monoclonal Antibodies , Inc., 802 F.2d 1367, 1384, 231 USPQ 81, 94 (Fed. Cir. 1986), cert. denied, 480 U.S. 947 (1987); Lindemann Maschinenfabrik GMBH v. American Hoist & Derrick Co., 730 F.2d 1452, 1463, 221 USPQ 481, 489 (Fed. Cir. 1984).

A full length sequence of GMPase is not required to enable the present invention, as embodied in the claims. Instead, the Applicant has satisfied the enablement requirement, since one of ordinary skill in the art would not be required to perform undue experimentation in order to practice the invention.

The Examiner maintains that the claims are broadly drawn to a method of increasing the endogenous level of vitamin C in a plant by expression of a nucleic acid that encodes an enzyme in a plant biosynthetic pathway for vitamin C biosynthesis, and plants thereby obtained. The Examiner rejects the claims on the grounds that the specification does not provide guidance for the sequence of the full-length gene encoding GMPase, for wild-type plants transformed with the GMPase gene, for methods of making stress resistant plants by transformation with a nucleic acid encoding the GMPase gene. The Examiner also asserts that plants transformed with the genes encoding the enzymes in the claims would not increase Vitamin C biosynthesis. On this basis, the Examiner maintains that undue experimentation would be required for one of ordinary skill in the art to practice Applicant's invention. Applicant respectfully traverses the Examiner's assertions.

The Applicant would like to respectfully point out that the enablement requirement applies to the claimed subject matter. "All questions of enablement are evaluated against the

claimed subject matter. The focus of the examination inquiry is whether everything within the scope of the claim is enabled." (M.P.E.P. 2164.08). Here, the claims do not claim the "sequence of the full-length gene" or "wild-type plants". Therefore, the Examiner's rejections on these bases are improper.

The specification provides ample guidance for the gene encoding GMPase

Applicant submits herewith its Declaration under 37 C.F.R. § 1.132, providing additional evidence in support of the arguments herein, showing that one of ordinary skill in the art would be able to practice the claimed invention without undue experimentation. See attached Declaration of Dr. Patricia Conklin. A copy of this declaration was provided to the Examiner prior to the telphone interview.

The present application provides ample guidance for the full-length sequence, and repeatable methods for cloning and sequencing the full-length gene encoding GMPase.

According to the application, mapping data indicated vtc1 mapped below marker m429 (using marker CAPS 178). (see present application, page 10, lines 10-25). Less ^{14}C-mannose was incorporated into AsA in vtc1 than wildtype and vtc1 had less mannose in the cell wall. (see present application, page 9, line 17 through page 10, line 6). See paragraphs 13 and 14 of Dr. Conklin's declaration.

An EST (EST ID #9908, Genbank #T46445) annotated as a "putative mannose-1-phosphate guanyltransferase " was subsequently found (see present application, page 11, lines 5-6). See paragraph 15 of Dr. Conklin's declaration. Since the EST is in the application, no experimentation would be required for someone skilled in the art to identify it.

In addition, the cDNA encoding the *Arabidopsis* GDP-mannose pyrophosphorylase (EST ID #9908, GenBank #T46645, www.ncbi.nlm.nih.gov/irx/cgi-bin/birx_doc?dbest_cu+6850, now found at http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=2763316) is already on deposit and can easily be obtained from the Arabidopsis Biological Resource Center (http://www.biosci.ohio-state.edu/~plantbio/Facilities/abrc/abrchome.htm; Columbus, OH), as described in the specification.

The Applicant then found BAC T5I7 (AC00300), which aligned almost perfectly with the EST (see present application, page 9, lines 25-29). This BAC is listed in the application. Attached is a printout of a BLAST query, which is dated 10-29-97. A copy of the BLAST query was provided to the Examiner prior to the telphone interview. See paragraph 19 of Dr. Conklin's Declaration. Clearly the sequence BAC T5I7 was available and annotated as "one ordered piece" as of that date. This BAC T517 is clearly identified in the application, and would allow someone skilled in the art to practice the invention without undue experimentation. The sequence of this BAC is not required in order for someone skilled in the art to practice the invention without undue experimentation. See paragraph 19 of Dr. Conklin's declaration.

The BAC T517 that the Examiner is requesting the sequence for was clearly identified in the application. "The sequence of a 92 kb BAC (T5I7) within that contig (Figure 3B) was annotated by TIGR and the open reading frame T5I7.7 was identified as a putative mannose-1-phosphate guanyltransferase (www.tigr.org/docs/tigr-scripts/bac_scripts/bac_display.spl?bac_name=T5I7)." (present application page 10, lines 25-28). The BAC is still available. The current URL is http://www.tigr.org/tigr-scripts/euk_manatee/BacAnnotationPage.cgi?db=ath1&asmbl_id=9934&page_size=27&page= and the current "locus number" for this gene is At2g39770. A printout for this website is attached. The Applicant used this BAC to further identify the VTC1 gene as GMPase. The disclosure of BAC T517 in the application would enable someone skilled in the art to practice the invention without undue experimentation. See paragraph 20 of Dr. Conklin's declaration.

"A 5.4 kb ClaI fragment containing the *VTC1* locus was subcloned from BAC T5I7. A 3.4 kb fragment from this subclone was then ligated into the binary vector pGPTV-BAR/HindIII by the said technique being known in the art, and incorporated by reference (Becker, D. *et al.* (1992) *Plant Mol. Biol.* 20, 1195-1197). This construct (g*VTC1*-pGPTV) was transformed into *Agrobacterium tumefaciens* pMP90 strain GV3101 and introduced into *vtc1-1* plants by vacuum infiltration." (present application page 14, lines 1-6).

In the telephone interview on April 13, 2004, the Applicant's agent explained that all that is needed to create the genetically engineered plant was identified and available at the time the application was filed.

The Examiner responded in the telephone interview that this was not enough to satisfy the enablement requirement. Instead, we would have to show that the entire sequence was available at the time of filing and stated that the BLAST query did not show the entire sequence. She said that in order to express the gene, we needed to show that the entire open reading frame was available. The gene was available at the time of filing, within the BACT517. A requirement that the sequence be known at the time of filing is not consistent with the law of enablement.

All that is needed is to show that someone skilled in the art could practice the claimed invention without undue experimentation. BACT517 is clearly identified in the application, and it was available at the time the application was filed. The size of the fragment used to create a subclone from BACT517 that contained VTC1, as well as the enzyme required to create the fragment, was disclosed in the application. The attached BLAST query shows that BACT517 was available to the public at the time of filing. This BAC is still readily available to the public at the ABRC. Therefore, someone skilled in the art clearly could practice the invention with little or no experimentation.

The Examiner stated in the telephone interview that we needed to show that the sequence was available at the time of filing, is still available today and would still be available 30 years from now. Clearly, the Applicant has shown that the BACT517 was available at the time of filing (see attached BLAST query, and present application Figure 3, and page 10, lines 26-30). The attached gene search results from the ABRC show that it is still available today. The Examiner is incorrect in requiring the Applicant to prove that the BACT517 must be available 30 years from now. "Unless there is a reasonable basis to believe that the biological material will cease to be available during the enforceable life of the patent, current availability would satisfy the requirement. The incentives provided by the patent system should not be constrained by the mere possibility that a disclosure that was once enabling would become non-enabling over a period of time through no fault of the patentee. *In re Metcalfe*, 410 F.2d 1378, 161 USPQ 789 (CCPA 1969)." (M.P.E.P. 2404.01). The Examiner has provided no evidence that BACT517.7 will cease to be available during the enforceable life of the patent. Therefore, since BACT517 is known and readily available today, there is no requirement that the Applicant prove that it would be available in 30 years.

Even if the Applicant conceded that the identification of the BACT517 and its use to subclone GMPase is not sufficient to enable the present invention (which the Applicant does not concede, see discussion above), it is respectfully submitted that Applicant's specification provides ample guidance for the full-length gene encoding GMPase. The specification recites that *VTC1* (which encodes the GMPase) was fine-mapped to a position on chromosome 2 to one side of two molecular markers; 0.9 cM from marker m429 and 1.2 cM from marker nga168 (as shown in Figure 3A). Using microsatellite marker 178, which is >1 cM centromeric proximal to nga168, it was determined that *VTC1* is centromere distal to nga168 and m429. (present application, page 10, lines 14-18). Applicant's mapping data place *VTC1* within a 2 Mb region on Chr 2 that spans m429 to just beyond marker m336. (present application, page 10, lines 23-24). Equipped with this mapping data, someone skilled in the art could take the steps to create a genetically engineered plant as recited in the claims without undue experimentation. The Applicant would like to remind the Examiner that the legal standard requires undue experimentation, not mere experimentation.

The foregoing data, taken together with the prior art, provide ample guidance for the full-length sequence, and repeatable methods for cloning and sequencing the full-length gene encoding GMPase, such that obtaining the full-length sequence would not require undue experimentation. See also paragraphs 11 and 13-21 of Dr. Conklin's Declaration.

Thus, Applicant's specification provides ample guidance for the full-length sequence, and repeatable methods for cloning and sequencing the cDNA and the full-length gene from BAC T517 encoding GMPase, such that one of ordinary skill in the art could practice the claimed invention without undue experimentation.

The specification provides ample guidance for plants transformed with a GMPase

It is respectfully submitted that Applicant's specification provides ample guidance for plants transformed with the GMPase gene, and for methods of making stress resistant plants by transformation with a nucleic acid encoding the GMPase gene. Indeed, Applicant's specification provides real examples of transgenic plants that Applicant, in fact, transformed with the full-length gene encoding GMPase (present application, page 14, lines 1-6), and which exhibited increased Vitamin C levels (present application, page 16, Table 1).

Applicant's specification need not (and preferably does not) disclose that which is well known in the art. In re Buchner, 929 F.2d 660, 661, 18 USPQ2d 1331, 1332 (Fed. Cir. 1991); In re Myers, 410 F.2d 420, 161 USPQ 668 (CCPA 1969); Lindemann Maschinefabrik GMBH v. American Hoist and Derrick Co., 221 USPQ 481 (Fed. Cir. 1984). The Examiner asserts that prior art by Bauw et al. (WO 98/50558) teaches *Arabidopsis* and tobacco plants transformed with a gene encoding L-galactono-y-lactone dehydrogenase (pages 15-20), an enzyme involved in vitamin C biosynthesis. The Examiner further asserts that increased vitamin C levels (Table 5) and increased stress resistance (page 2 lines 16-21) are inherent properties of these plants (office action dated July 24, 2001, page 9 line 21 to page 10 line 2).

Thus, the Examiner acknowledged in a prior office action that the prior art teaches that plants can be transformed with a gene encoding an enzyme in the Vitamin C pathway and thereby produce transgenic plants having increased Vitamin C and stress resistance.

Therefore, based on the extensive teachings in the art, combined with the teachings in Applicant's disclosure (which provides real examples), it is clear that a wide variety of plants can be transformed with a gene encoding an enzyme in the Vitamin C biosynthetic pathway, thereby increasing the levels of Vitamin C and the stress resistance of the plants. See paragraph 26 of Dr. Conklin's declaration.

Combined with the extensive teachings of the prior art, Applicant's disclosure provides ample guidance for wild-type plants transformed with the GMPase gene, and for methods of making stress resistant plants by transformation with a nucleic acid encoding the GMPase gene, such that producing the transgenic plants would not require undue experimentation.

Indeed, by following the teachings in its specification, Applicant subsequently has identified another locus for a gene potentially encoding another enzyme in the Vitamin C biosynthesis pathway, VTC4. See Ser. No. 09/909,600. The methods used were identical to those in the present specification. Thus, clearly, the present specification provides enablement for the claimed invention. See paragraph 22 of Dr. Conklin's declaration.

It is respectfully submitted that the Examiner's assertion that the unpredictability associated with expression of genes in plants has not been overcome is mistaken, in that

Applicant's gene encoding GMPase was, in fact, transformed into plants, thereby generating genetically engineered plants having increased levels of Vitamin C, relative to the progenitor plants. See Applicant's specification at page 13, line 24, through page 17, line 3. Thus, clearly, Applicant's GMPase can be expressed in plants, and clearly such plants have increased levels of Vitamin C, thus overcoming any alleged unpredictability.

The specification provides ample guidance that plants transformed with at least one of the enzymes in the claims has increased Vitamin C biosynthesis

The Examiner stated that "expression of a nucleic acid encoding any of the enzymes before galactono-1,4-lactone dehydrogenase [in] the vitamin C biosynthesis pathway shown in the instant Figure 1, including phosphoglucose isomerase, phosphomannomutase, GMPase, or GDP-mannose epimerase, would not increase vitamin C levels relative to those in wild-type plants." (present office action dated December 31, 2003, page 7, lines 4-8).

The Examiner has also stated that the application does not show a genetically engineered plant with increased Vitamin C biosynthesis. However, the application clearly provided data that a genetically engineered plant had increased levels of Vitamin C when compared to a progenitor plant.

"Rescue of the Mutant Phenotype by Creating A Recombinant Plant

By introducing the wild type version of the GDP-mannose pyrophosphorylase gene, the mutant phenotype should be rescued. In effect, the recombinant plant created via transformation will be able to functionally express recombinant GDP-mannose pyrophosphorylase and restore function.

A 5.4 kb ClaI fragment containing the *VTC1* locus was subcloned from BAC T5I7. A 3.4 kb fragment from this subclone was then ligated into the binary vector pGPTV-BAR/HindIII by the said technique being known in the art, and incorporated by reference (Becker, D. *et al.* (1992) *Plant Mol. Biol.* 20, 1195-1197). This construct (g*VTC1*-pGPTV) was transformed into *Agrobacterium tumefaciens* pMP90 strain GV3101 and introduced into *vtc1-1* plants by vacuum infiltration.

The vacuum filtration method for transformation is discussed below. The seeds are planted on top of window screen covered soils. After the plants have bolted, clip off the primary

bolt to encourage growth of secondary bolts. Perform infiltration around four days after clipping. Start a 20 ml overnight culture of Agrobacterium carrying the gVTC1-GPTV construct including the appropriate antibiotics (kan, rif, and gm) two days prior to transformation. The day before the transformation, use this overnight culture to inoculate a large (~500 ml) culture. After 24 hrs of growth, harvest cells by centrifugation and wash once with growth media without antibiotics. Resuspend bacteria at 0.8 OD units in infiltration media. One liter of infiltration media consists of 0.5X MS salts, 1X B5 vitamins, 5% sucrose, 0.044 uM benzylamino purine, 0.03% Silwet L-77, and 0.5 g MES (pH to 5.7 with KOH). Pour some of diluted bacteria into a rubbermaid dish that fits inside the vacuum oven (be sure to turn oven temperature off prior to use). Invert pot with plants to be infiltrated into culture and place in vacuum oven. Infiltrate 5-10 min at 15 in^3 Hg. The vacuum is not necessary as just dipping the plants into the culture for ~5 min also gives similar transformation frequency. For the p*VTC1*-pGPTV infiltrations, both vacuum infiltration and dipping alone produced similar results. Release the vacuum and remove the pot. Cover with plastic wrap and return to the light room. Remove the cover the next day. A newer streamlined procedure being known in the art, and incorporated by reference (S.J. Clough and A.F. Bent, 1998. *Plant J.* **16**:735-743) can alternatively be used for transformation.

Glufosinate-ammonium resistant T_1 transgenic individuals were selected by sowing seeds and spraying the soil surface with 500 ml per m^2 of 0.25 mg ml^{-1} commercially formulated glufosinate-ammonium (Finale; AgrEvo, Montvale NJ). Twelve days after sowing, resistant T_1 seedlings were transplanted to nontreated soil and allowed to self-pollinate.

T_2 progeny were scored for glufosinate-ammonium resistance by painting individual leaves with the herbicide (150 μg ml^{-1} glufosinate-ammonium, 250 nl ml^{-1} Silwet). These plants were also scored for wildtype or mutant (deficient) levels of AsA by a nitroblue tetrazolium-based method in which single leaves are squashed onto chromatography paper and treated with 1mg/ml of nitroblue tetrazolium. The AsA in wildtype leaves is sufficient to reduce the nitroblue tetrazolium to the visible precipitate formazan, while no readily visible formazan is produced upon treatment of *vtc1-1* leaves (Conklin *et al.*, in preparation). AsA levels were then confirmed by a previously described spectrophotometric-based assay (Conklin, P.L. *et al.* (1996) *Proc. Natl. Acad. Sci.* USA **93**, 9970-9974). (Table 1 omitted).

If the VTC1 locus encodes GDP-mannose pyrophosphorylase, a wildtype copy of this locus introduced as a transgene will complement the *vtc1-1* allele and restore normal levels of AsA. To test this hypothesis, a genomic clone including ~ 1.1 kb upstream of the 5' end of the GDP-mannose pyrophosphorylase cDNA and ~0.2 kb downstream of the predicted stop codon (Figure 3c) was subcloned from BAC T5I7 and transformed into *vtc1-1* plants by the *Agrobacterium tumefaciens* vacuum infiltration method. T_1 transgenic plants were selected by

glufosinate-ammonium resistance conferred by the BAR gene. Thirteen glufosinate-ammonium resistant T_1 transgenics that were confirmed to contain the BAR gene by PCR-amplication all contained wildtype levels of AsA. These results were consistent with the hypothesis that the transgene complemented *vtc1-1*. The T_1 lines were allowed to self-pollinate and three selected T_2 lines from independent T_1 lines were tested for co-segregation of wildtype levels of AsA (scored using a qualitative AsA assay) and glufosinate-ammonium resistance. Introduction of the *VTC1* locus into the AsA-deficient *vtc1-1* mutant confers increased levels of AsA that co-segregate with the selectable marker (Table 1). Finally, ten individuals that scored as wildtype for AsA from each T_2 line were pooled, extracts were prepared, and total AsA was measured using a quantitative spectrophotometric assay. These pooled extracts contained between 2.4 and 3.8 μmoles AsA/g FWT of AsA which is similar to the 3.1 μmoles AsA/g FWT seen in wildtype, and greater than the 0.9 μmoles AsA/g FWT in the mutant. Together, these results confirm that the *VTC1* locus encodes a GDP-mannose pyrophosphorylase structural gene." (present application, page 13, line 24 to page 17, line 2).

The Examiner states that, since this is complementation analysis, the data is not persuasive. In the telephone interview, the Examiner stated that the complementation experiments provide no utility for the present invention. Applicant would like to point out that the Examiner did not make a utility rejection in the present office action.

As discussed above, the Applicant is only required to enable the claimed subject matter. In this application, the Applicant has enabled the claims, as written, by showing a genetically engineered plant comprising a recombinant nucleic acid that encodes an enzyme in a plant Vitamin C biosynthesis pathway, wherein the enzyme is selected from the group consisting of phosphoglucose isomerase, phosphomannomutase, GDP-mannose pyrophosphorylase, and GDP-D-mannose-3,5-epimerase This is exactly what is claimed in claim 1. The Examiner can not just decide that the example given is not adequate, when it specifically enables the subject matter claimed.

The Examiner stated, in an earlier office action that "Trulson [6,143,562] et al teach tomato, melon, squash and maize plants transformed with a gene encoding phosphomannose isomerase, ...an enzyme in the vitamin C biosynthetic pathway. The claimed increased stress resistance would have been an inherent property of these plants, as would increased vitamin C levels....Trulson et al disclose various dicots transformed with a gene encoding phosphomannose isomerase..., an enzyme in the vitamin C biosynthetic pathway; these plants would have

increased stress resistance and vitamin C levels." (office Action dated July 24, 2001 page 9, section 15, lines 15-19 and page 10, lines 14-16).

In the current office action, the Examiner completely changes her position, and states that "this is not found persuasive because, in light of the teachings of Gatzek et al., plants transformed with a nucleic acid encoding phosphomannose isomerase would not inherently have increased vitamin C levels and increased stress resistance." (present office action dated December 31, 2003, page 10, lines 4-6). Applicant respectfully traverses this assertion, and requests additional evidence from the Examiner to support her arguments that the Gatzek results nullify what she previously stated was inherently disclosed in Trulson.

Gatzek et al. only show that an increase in enzyme levels for L-galactose dehydrogenese did not increase Vitamin C concentration in leaves in their experiments (see abstract). The Davey reference merely shows that there is more than one Vitamin C biosynthesis pathway. The Agius reference shows that overexpression of an enzyme in one of the other pathways can increase Vitamin C biosynthesis. The Examiner concludes from the results in these references that "expression of a nucleic acid encoding any of the enzymes before galactono-1,4-lactone dehydrogenase [in] the vitamin C biosynthesis pathway shown in the instant Figure 1, including phosphoglucose isomerase, phosphomannomutase, GMPase, or GDP-mannose epimerase, would not increase vitamin C levels relative to those in wild-type plants." (present office action dated December 31, 2003, page 7, lines 4-8). The Examiner expanded on the reasons for her conclusion in the telephone interview. She stated that, since one of the enzymes in our pathway was unable to increase levels of Vitamin C, it was fair to conclude that none of the enzymes in the pathway of the present invention were capable of increasing Vitamin C biosynthesis. She stated that Applicant was required to show how their enzyme(s) were different than the enzyme in Gatzek.

However, this conclusion is entirely unwarranted by the evidence. The Examiner has provided no concrete evidence for the record to support the conclusion she makes based on the results in the Gatzek paper. An equally plausible conclusion from the Gatzek results is that the rate-limiting step is before the galactono-1,4, lactone dehydrogenase in the pathway of the present invention. This alternate explanation would also account for the results from the Gatzek

et al. paper. In fact, as discussed above, in earlier office actions, the Examiner made completely contrary statements as applied to the Trulson and Bauw references. In addition, plants transformed with GMPase in the present application do have increased Vitamin C levels compared to the progenitor plants. Therefore, the Applicant respectfully requests that the Examiner provide additional evidence to support her conclusion that the expression of a nucleic acid encoding the enzymes listed in the claims actually do not increase Vitamin C biosynthesis, instead of merely providing indirect evidence and unsupported inferences.

The Examiner is essentially arguing that the overexpression of the enzymes listed in the claims may not increase Vitamin C biosynthesis in all situations. However, even if this were true (which the Applicant does not concede), the Applicant has enabled the invention, by providing a real example, which supports the claims, as currently written.

In view of the foregoing amendments and remarks, Applicant respectfully submits that these amendments have fully addressed the Examiner's rejections, and that the claims are now in condition for allowance. Reconsideration and withdrawal of the rejection of claims 1-22 and 24-26 as lacking enablement are respectfully requested.

7. Claims 1-22 and 24-26 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. Applicant respectfully disagrees with the rejection, and believes that the specification provides an adequate written description of the claimed subject matter, such that one of ordinary skill in the art would understand that Applicant had possession of the invention at the time of filing.

The test for compliance with the written description requirement is whether the disclosure as originally filed reasonably conveys to the artisan that the inventor had possession at that time of the later claimed subject matter, rather than the presence or absence of literal support in the specification for the claim language. Ralston Purina Co. v. Far-Mar-Co., Inc., 772 F.2d 1570, 1575, 227 USPQ 177, 179 (Fed. Cir. 1985) (quoting In re Kaslow, 707 F.2d 1366, 1375, 217 USPQ 1089, 1096 (Fed. Cir. 1983). The standard is whether the written description allows

persons of ordinary skill in the art to recognize that the patent applicant invented what is claimed. In re Gosteli, 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989).

Whenever the issue arises, **the fundamental factual inquiry is whether a claim defines an invention that is clearly conveyed to those skilled in the art at the time the application was filed**. However, the subject matter of the claim need not be described literally (*i.e.*, using the same terms or *in haec verba*) in order for the disclosure to satisfy the description requirement. See In re Kaslow, 707 F.2d 1366, 1375, 217 USPQ 1089, 1096 (Fed. Cir. 1983). Further, the disclosure must be read in light of the knowledge of those skilled in the art, as evidenced by references available to the public prior to the filing date. In re Lange, 644 F.2d 856, 863, 209 USPQ 288, 294 (CCPA 1981).

The purpose of the written description requirement is to prevent an applicant from later asserting that he invented that which he did not. Compliance with the written description requirement is essentially a fact-based inquiry that will "necessarily vary depending on the nature of the invention claimed." Enzo Biochem v. Gen-Probe, Inc., 296 F.3d 1316, 1324, 63 USPQ2d 1609, 1613 (Fed. Cir. 2002). In Enzo Biochem, the Federal Circuit clarified that Eli Lilly did not hold that all functional descriptions of genetic material necessarily fail as a matter of law to meet the written description requirement; rather, the requirement may be satisfied if in the knowledge of the art the disclosed function is sufficiently correlated to a particular, known structure. See Enzo Biochem, 296 F.3d at 1324, 63 USPQ2d at 1613 (emphasis added).

More recently, the Federal Circuit has clearly stated that:

> "We held in Eli Lilly that the adequate description of claimed DNA requires a precise definition of the DNA sequence itself — not merely a recitation of its function or a reference to a potential method for isolating it. 119 F.3d at 1566-67, 43 USPQ2d at 1406 (holding the disclosure of the cDNA sequence of the insulin gene of a rat did not adequately describe the cDNA sequence of the insulin gene of every vertebrate). More recently, in Enzo Biochem, we clarified that Eli Lilly did not hold that all functional descriptions of genetic material necessarily fail as a

> matter of law to meet the written description requirement; rather, the requirement may be satisfied if in the knowledge of the art the disclosed function is sufficiently correlated to a particular, known structure. See Enzo Biochem, 296 F.3d at 1324, 63 USPQ2d at 1613."

See Amgen v. Hoescht Marion Roussel, Inc., 65 USPQ2d 1385 (Fed. Cir. 2003).

It is respectfully submitted that many of the genes encoding GMPase (including that of *Arabidopsis* and other species), as well as most of the other enzymes in the Vitamin C pathway, are well known in the art and, as such, are not required to be disclosed in Applicant's specification. Furthermore, Applicant's Figure 1 and the specification at page 4, lines 12-16, disclose the enzymes in the Vitamin C pathway.

Further, Applicant's specification provides ample guidance for the sequence of the gene encoding GMPase, as explained above. The Applicant clearly had possession of the claimed invention, as evidenced by the identification and usage of BACT517 to obtain a subclone containing VTC1. Thus, one of ordinary skill in the art would know that Applicant was in possession of the GMP-mannose pyrophosphorylase gene and recombinant plants transformed with this gene that express increased levels of Vitamin C.

Applicant submits herewith its Declaration under 37 C.F.R. § 1.132, providing additional evidence in support of the foregoing arguments, showing that one of ordinary skill in the art would understand that Applicant was in possession of the GMP-mannose pyrophosphorylase gene and recombinant plants transformed with this gene that express increased levels of Vitamin C. See paragraphs 27 through 30 of Dr. Conklin's declaration.

In view of the foregoing amendments and remarks, Applicant respectfully submits that these amendments have fully addressed the Examiner's rejections, and that the claims are now in condition for allowance. Reconsideration and withdrawal of the rejection of claims 1-22 and 24-26 as lacking a sufficient written description are respectfully requested.

8. Claims 1-8, 10, 16-22 and 24-26 were rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. Applicant respectfully disagrees with the rejections.

In reviewing a claim for compliance with 35 U.S.C. 112, second paragraph, the Examiner must consider the claim as a whole, in light of the specification and the knowledge of the prior art, to determine whether the claim apprises one of ordinary skill in the art of its scope and, therefore, serves the notice function required by 35 U.S.C. 112, second paragraph, by providing clear warning to others as to what constitutes infringement of the patent. See, *e.g.*, Solomon v. Kimberly-Clark Corp., 216 F.3d 1372, 1379, 55 USPQ2d 1279, 1283 (Fed. Cir. 2000). A claim is indefinite only if, when read in light of the specification, it is "insolubly ambiguous, and no narrowing construction can properly be adopted." Exxon Research & Eng'g Co. v. United States, 265 F.3d 1371, 1375, 60 USPQ2d 1272, 1276 (Fed. Cir. 2001); Allen Eng'g Corp. v. Bartell Indus., Inc., 299 F.3d 1336, 1349, 63 USPQ2d 1769, 1776 (Fed. Cir. 2002).

The Examiner continues to maintain that claim 1 is indefinite for its recitation of "plant Vitamin C biosynthesis pathway." In the telephone interview, the Examiner explained that she believes that the language of the claim is too broad. The Applicant respectfully disagrees. The enzymes deemed to be encompassed by the claims are described throughout Applicant's specification, such as, for example, at Figure 1. The source of the nucleic acids that encode these enzymes is not relevant, particularly since Applicant's claims do not have any limitations regarding the source of the nucleic acid. Rather, the claims are limited merely to the specific proteins recited having the described enzymatic activity. In addition, the fact that plants may have more than one possible Vitamin C pathway is irrelevant, since the specific enzymes being claimed are listed in claim 1. Therefore, claim 1 is definite. Thus, one of ordinary skill in the art would understand what is claimed, when the claims are read in light of the specification. See paragraph 31 of Dr. Conklin's declaration. Reconsideration and withdrawal of the rejection of claim 1 is respectfully requested.

The Examiner maintains that claims 2 and 10 are indefinite in their recitation of "said plant, or portion thereof, is a dicot." Although Applicant respectfully disagrees, claims 2 and 10 have been amended to further prosecution of the application. Reconsideration and withdrawal of the rejection of claims 2 and 10 is respectfully requested.

The Examiner maintains that the relative term "increasing" in claim 16 renders the claim indefinite. Applicant respectfully disagrees.

Definiteness problems often arise when words of degree are used in a claim. That some claim language may not be precise, however, does not automatically render a claim invalid. The question becomes whether one of ordinary skill in the art would understand what is claimed when the claim is read in light of the specification. See generally Anchor Wall Systems, Inc. v. Rockwood Retaining Walls, Inc., (Fed. Cir. No. 02-1592, 2003).

A person of ordinary skill in the art would understand the meaning of the term "increasing" and apply its plain, ordinary meaning. There is no requirement for Applicant to define this term, as it is a term that is known to virtually everyone and its meaning is quite clear. More particularly, one of ordinary skill in the art would understand that the claimed transgenic plants have increased Vitamin C relative to plants that are not so transformed. See paragraph 32 of Dr. Conklin's declaration. Reconsideration and withdrawal of the rejection of claim 16 is respectfully requested.

Double Patenting Rejection

10. Claims 1-22 and 24-26 were provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-23 and 27 of copending Application No. 09/909,600. Applicant respectfully disagrees.

Since this is a provisional obviousness-type double patenting rejection, the Applicant is not required to act at this time. In addition, application serial number 09/909,600 has been abandoned, and therefore the rejection is now moot. Reconsideration and withdrawal of the rejection is respectfully requested.

Conclusion

Applicant believes the claims, as amended, are patentable over the prior art, and that this case is now in condition for allowance of all claims therein. Such action is thus respectfully requested. If the Examiner disagrees, or believes for any other reason that direct contact with Applicant's attorney would advance the prosecution of the case to finality, he is invited to telephone the undersigned at the number given below.

"Recognizing that Internet communications are not secured, I hereby authorize the PTO to communicate with me concerning any subject matter of this application by electronic mail. I understand that a copy of these communications will be made of record in the application file."

Respectfully Submitted:
Conklin et al.

By: _____
Meghan Van Leeuwen, Reg. No. 45,612
Agent for Applicant

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Dated: 4/20/04

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THE INSTITUTE FOR GENOMIC RESEARCH

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arabidopsis thaliana

Gene content for T5I7

Annotation Database

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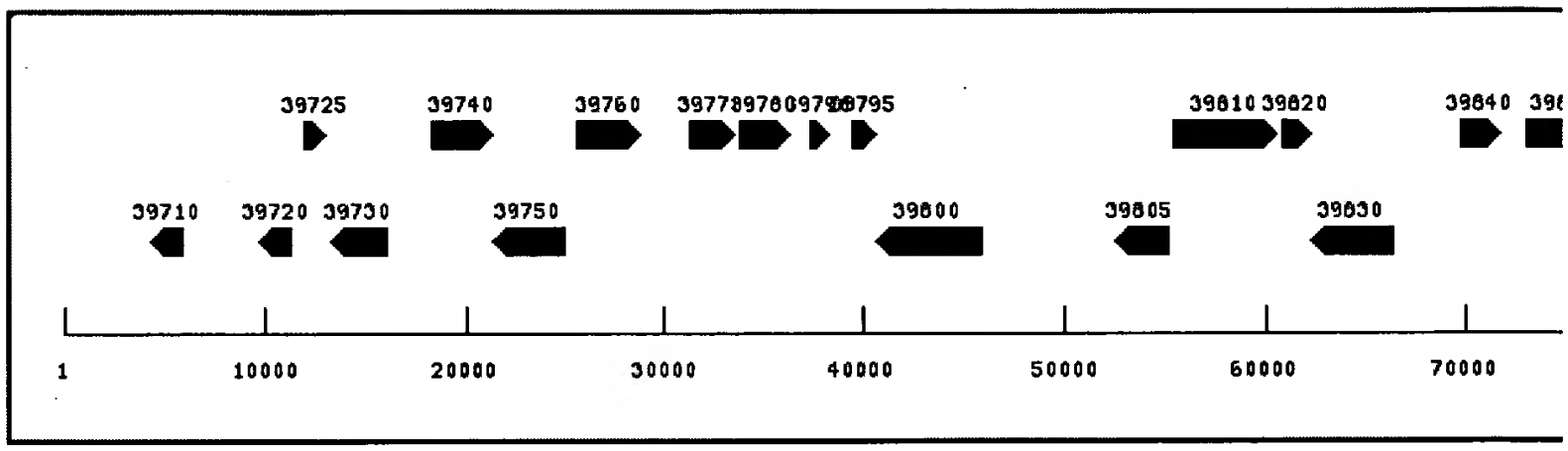
Locus Search
Sequence Search
HMM Search

Arabidopsis Links

BAC Tiling Path

Download Sequences



PAGE 1 OF 1 ...[List all]

Locus	5' coordinate	3' coordinate	Gene product name
At2g39710	5913	4321	aspartyl protease family protein
At2g39720	11355	9742	zinc finger (C3HC4-type RING finger) family protein
At2g39725	11963	13082	complex 1 family protein / LVR family protein
At2g39725	11963	13082	complex 1 family protein / LVR family protein
At2g39730	16081	13279	ribulose bisphosphate carboxylase/oxygenase activase / RuBisCO activase
At2g39730	16081	13279	ribulose bisphosphate carboxylase/oxygenase activase / RuBisCO activase
At2g39730	16081	13279	ribulose bisphosphate carboxylase/oxygenase activase / RuBisCO activase
At2g39740	18308	21350	expressed protein
At2g39750	24937	21357	dehydration-responsive family protein
At2g39760	25620	28785	speckle-type POZ protein-related
At2g39770	31238	33518	GDP-mannose pyrophosphorylase (GMP1)
At2g39780	33774	36280	ribonuclease 2 (RNS2)

At2g39790	37366	38333	mitochondrial glycoprotein family protein / MAM33 family protein
At2g39795	39520	40695	mitochondrial glycoprotein family protein / MAM33 family protein
At2g39800	45852	40697	delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1)
At2g39800	45852	40697	delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1)
At2g39805	55050	52464	integral membrane Yip1 family protein
At2g39810	55365	60590	expressed protein
At2g39820	60810	62222	eukaryotic translation initiation factor 6, putative / eIF-6, putative
At2g39830	66293	62310	LIM domain-containing protein
At2g39840	69791	71822	serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1
At2g39850	73159	76786	subtilase family protein
At2g39855	80210	81841	expressed protein
At2g39855	80210	81841	expressed protein
At2g39870	86076	87910	expressed protein
At2g39880	92012	90478	myb family transcription factor (MYB25)

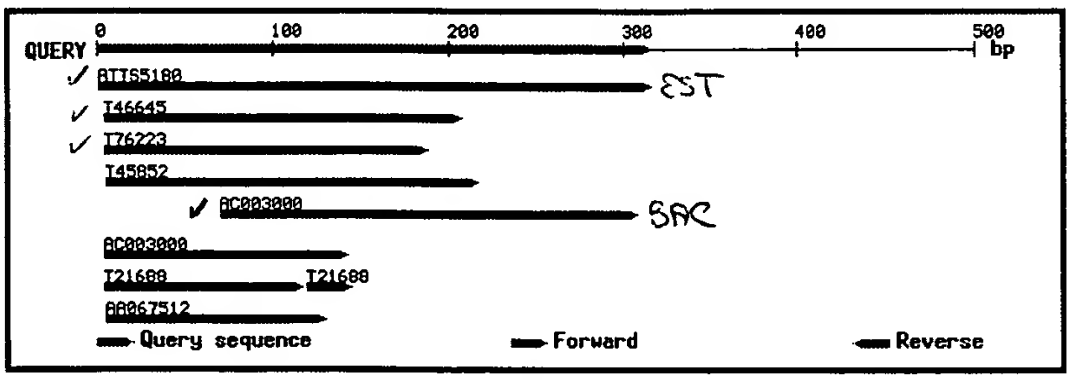
PAGE 1 OF 1 ...[List all]

Arabidopsis Comments/Questions

Patrick Cahill

10-29-97

Summary of BLAST to Arabidopsis GenBank DNA sequences using a minimum match cutoff of 50%.



Full length cDNA should be ≈ 125.2 ~~234~~ bp ~363 aa

The full results of this search are below.

BLAST query on *Arabidopsis* sequences

Query performed by the Arabidopsis thaliana Database ; for full BLAST options and parameters, refer to the NCBI BLAST Documentation

224 EE277

Links to GenBank, EMBL, PIR, and SwissProt are shown in **bold** type; links to locations within this document are in normal type.

Your comments and suggestions are requested: Send a Message to AtDB

BLASTN 2.0a9MP-WashU [12-May-1997] [Build 13:37:35 May 13 1997]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query Sequence: No sequence name provided. (Length: 311)

Database: *Arabidopsis* GenBank Data Set; 53,069 sequences; 43,739,919 total letters.

Sequences producing High-scoring Segment Pairs:

		High Score	Smallest Sum Probability P(N)	N
GenBank | ATTS5180 | F14258 A. thaliana transcribed sequence;...		1506	3.0e-120	1
GenBank | AC003000 | AC003000 *** SEQUENCING IN PROGRESS *** ...		815	2.0e-106	3
GenBank | T46645 | T46645 9908 Arabidopsis thaliana cDNA cl...		972	1.7e-75	1
GenBank | T45852 | T45852 9115 Arabidopsis thaliana cDNA cl...		704	4.6e-70	2
GenBank | T76223 | T76223 11001 Arabidopsis thaliana cDNA c...		852	5.9e-66	1
GenBank | T21688 | T21688 3696 Arabidopsis thaliana cDNA cl...		529	7.3e-40	2
GenBank | AA067512 | AA067512 26373 Lambda-PRL2 Arabidopsis t...		312	6.9e-27	2

Vaucheret, Gary Thornburg & Kobmann Furbank

EST's in UTC1 Contig against (11 EST (ATTS5180)

ATTS5180|F14258 A. thaliana transcribed sequence; clone OBO32; 5' end. [GenBank / EMBL]
6/95
Length = 311

Plus Strand HSPs:

Score = 1506 (416.1 bits), Expect = 3.0e-120, P = 3.0e-120
Identities = 304/311 (97%), Positives = 304/311 (97%), Strand = Plus / Plus

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Sbjct:      1 GAGGACCATTGACTCTCAGTTTCCCAAAGCCCCTTGTTGATTTTGCTAATAAACCCATGA 60

Query:     61 TCCTTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     61 TCCTTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCA 120

Query:    121 ATTATCAGCCAGAGGTGATGCTGAACTTCTTGAAGGACTTTNAGACCAAGCTGGAAATCA 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
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Query:    181 AAATCACTTGCTCACAAGAGACCGAGCCACTAGGTACCNCTGGTCCTCTNGCTCTAGCGA 240
              |||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
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Query:    241 GAGACAAATTGCTTGATGGATCTNGAGAGNCCTTCTTTGTTCTTAACAGTGATGTGNTTA 300
              |||||||||||||||||||||| ||||| ||||||||||||||||||||||||| |||
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Query:    301 GTGGNGTACCC 311
              |||| ||||||
Sbjct:    301 GTGGNGTACCC 311
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AC003000|AC003000 *** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T5I7' genomic sequence near marker 'CIC10A06'; HTGS phase 2, 1 ordered pieces. 10/97 [GenBank / EMBL]
Length = 115,000

Plus Strand HSPs:

Score = 815 (225.2 bits), Expect = 2.0e-106, Sum P(3) = 2.0e-106
Identities = 167/175 (95%), Positives = 167/175 (95%), Strand = Plus / Plus

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Query:   189 TGCTCACAAGAGACCGAGCCACTAGGTACCNCTGGTCCTCTNGCTCTAGCGAGAGACAAA 248
            |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
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Query:   249 TTGCTTGATGGATCTNGAGAGNCCTTCTTTGTTCTTAACAGTGATGTGNTTAGTG 303
            |||||||||||||| ||||| |||||||||||||||||||||||| ||||||
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 Score = 356 (98.4 bits), Expect = 2.0e-106, Sum P(3) = 2.0e-106
 Identities = 76/82 (92%), Positives = 76/82 (92%), Strand = Plus / Plus

Query:     4 GACCATTGACTCTCAGTTTCCCAAAGCCCCTTGTTGATTTTGCTAATAAACCCATGATCC 63
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query:    64 TTCATCAGATAGAGGCTCTTAA 85
            |||||||| ||      ||||||
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 Score = 336 (92.8 bits), Expect = 2.0e-106, Sum P(3) = 2.0e-106
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Query:   130 CAGAGGTGA 138
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T46645|T46645 9908 Arabidopsis thaliana cDNA clone 139E19T7. 8/95        [GenBank / EMBL]
          Length = 544

  Plus Strand HSPs:

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 Identities = 196/199 (98%), Positives = 196/199 (98%), Strand = Plus / Plus

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Query:    64 TTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCAATT 123
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Query:   184 TCACTTGCTCACAAGAGAC 202
            |||||||||||||||| |
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Query:     5 ACCATTGACTCTCAGTTTCCCAAAGCCCCTTGTTGATTTTGCTAATAAACCCATGATCCT 64
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Sbjct:   195 ACCATTGACTCTNAGTTTCCCAAAGCCCCTTGTTGATTTTCCTAATAAACCCATGATCCT 254

Query:    65 TCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCAATTA 124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query:   125 TCAGCCAGAGGTGATGCTGAACTT 148
            ||||||||||||||||||||||||
Sbjct:   315 TCAGCCAGAGGTGATGCTGAACTT 338

 Score = 251 (69.4 bits), Expect = 4.6e-70, Sum P(2) = 4.6e-70
 Identities = 55/65 (84%), Positives = 55/65 (84%), Strand = Plus / Plus

Query:   147 TTCTTGAAGGACTTTNAGACCAAGCTGGAAATCAAAATCACTTGCTCACAAGAGACCGAG 206
            |||||||||||||||  |  |||||||| |||||||||||||||| ||||||| | ||| |
Sbjct:   338 TTCTTGAAGGACTTTNNGNNCAAGCTGGNAATCAAAATCACTTGNTCACAAGGGGCCGNG 397

Query:   207 CCACT 211
            ||||
Sbjct:   398 NCACT 402


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          Length = 403

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Query:    64 TTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCAATT 123
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Sbjct:   195 TTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCCATCAATT 254

Query:   124 ATCAGCCAGAGGTGATGCTGAACTTCTTGAAGGACTTTNAGACCAAGCTGGAAATCAAAA 183
            |||||||||||||||||||||||||||||||||||| |||||||||||| ||   |||
Sbjct:   255 ATCAGCCAGAGGTGATGCTGAACTTCTTGAAGGACTTTNAGACCAAGCTGGNAAATCAAA 314


T21688|T21688 3696 Arabidopsis thaliana cDNA clone 96N23T7. 7/95        [GenBank / EMBL]
          Length = 464

  Plus Strand HSPs:

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Query:     4 GACCATTGACTCTCAGTTTCCCAAAGCCCCTTGTTGATTTTGCTAATAAACCCATGATCC 63
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   195 GACCATTGACTCTNAGTTTCCCAAAGCCCCTTGTTGATTTTGCTAATAAACCCATGATCC 254
```

```
Query:    64 TTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTT 112
             ||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct:   255 TTCATCAGATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGGTTT 303

 Score = 96 (26.5 bits), Expect = 7.3e-40, Sum P(2) = 7.3e-40
 Identities = 20/21 (95%), Positives = 20/21 (95%), Strand = Plus / Plus

Query:   120 AATTATCAGCCAGAGGTGATG 140
             | ||||||||||||||||||
Sbjct:   314 ATTTATCAGCCAGAGGTGATG 334


AA067512|AA067512 26373 Lambda-PRL2 Arabidopsis thaliana cDNA clone      [GenBank / EMBL]
            92D9T7. 9/96
            Length = 318

  Plus Strand HSPs:

 Score = 312 (86.2 bits), Expect = 6.9e-27, Sum P(2) = 6.9e-27
 Identities = 64/67 (95%), Positives = 64/67 (95%), Strand = Plus / Plus

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             |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||| ||
Sbjct:   196 ACCATTGACTCTAAGTTTCCCAAAGCCCCTTGTTGATTTTNCTAATAAACCCATGATNCT 255

Query:    65 TCATCAG 71
             |||||||
Sbjct:   256 TCATCAG 262

 Score = 176 (48.6 bits), Expect = 6.9e-27, Sum P(2) = 6.9e-27
 Identities = 40/46 (86%), Positives = 40/46 (86%), Strand = Plus / Plus

Query:    71 GATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAGTGGTTTTGGCC 116
             |||||||||||||||||||||||||||||||||   | ||| | |
Sbjct:   263 GATAGAGGCTCTTAAGGCAGTTGGAGTTGATGAAAGTGGTTTTGGC 308

 Score = 99 (27.4 bits), Expect = 1.4e-20, Sum P(2) = 1.4e-20
 Identities = 21/23 (91%), Positives = 21/23 (91%), Strand = Plus / Plus

Query:   103 AAGTGGTTTTGGCCATCAATTAT 125
             |||||||||||||||||| || |
Sbjct:   296 AAGTGGTTTTGGCCATCANTTTT 318


Parameters:
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  V=100
  nogap

  ctxfactor=2.00
  E=10

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   -1      0   +5,-4           0.192   0.173    0.357     same     same     same

  Query
  Strand MatID  Length  Eff.Length    E      S  W   T  X      E2  S2
   +1      0     311       304      10.  104 11 N/A 73   0.021 76
   -1      0     311       304      10.  104 11 N/A 73   0.021 76

Statistics:

  Database:  /share/fasolt/gcg5/gcgdata/gcgblast//ArabidopsisN
    Title:  ArabidopsisN
    Release date:  unknown
    Posted date:  2:54 AM PST Oct 28, 1997
    Format:  BLAST
  # of letters in database:  43,739,919
  # of sequences in database:  53,069
  # of database sequences satisfying E:  7
  No. of states in DFA:  196 (392 KB)
  Total size of DFA:  404 KB (448 KB)
  Time to generate neighborhood:  0.01u 0.00s 0.01t  Elapsed: 00:00:00
  No. of processors used:  2
  Search cpu time:  2.41u 1.56s 3.98t  Elapsed: 00:00:07
  Total cpu time:  2.58u 1.71s 4.30t  Elapsed: 00:00:09
  Start:  Wed Oct 29 08:25:23 1997   End:  Wed Oct 29 08:25:32 1997
```

TAIR Gene Search Results

new search
new gene search

download
check the boxes below and download results

Your query for genes where gene name, locus name or GenBank accession matches exactly the term At2g39770 resulted in 1 locus match with 5 distinct gene model.

Displaying 1 - 1.

To see ESTs associated with your gene of interest, click on the Locus link.

Check All | Uncheck All

	Locus	Gene Model	Description	Other Names (type)	full-length cDNA	Keywords
1 ☐	AT2G39770	AT2G39770.1	GDP-mannose pyrophosphorylase (GMP1), identical to GDP-mannose pyrophosphorylase from Arabidopsis thaliana (GI:3598958); updated per Conklin PL et al, PNAS 1999, 96 (7):4198-203	T5I7.7(orf) T5I7_7(orf) AT2G39770(orf)	yes	mitochondrion, nucleotidyltransferase activity, biosynthesis
	CYT1		putative mannose-1-phosphate guanyltransferase	CYTOKINESIS DEFECTIVE 1(full_name)	yes	mannose-1-phosphate guanylyltransferase activity, cellulose biosynthesis
	EMB101			EMBRYO DEFECTIVE 101(full_name)	yes	
	GMP1		GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds	GDP-MANNOSE PYROPHOSPHORYLASE 1(gene_product) GDP-MANNOSE PYROPHOSPHORYLASE 1(full_name)	yes	
	VTC1			SOZ1(symbol) VITAMIN C DEFECTIVE 1 (full_name)	yes	

General comments or questions: **curator@arabidopsis.org**
Seed or DNA stock questions (donations, availability, orders, etc): **abrc@arabidopsis.org**

Locus: AT2G39770

Date last modified 2003-05-02

TAIR Accession Locus:2005504

Representative Gene Model AT2G39770.1

Other names: CYT1, CYTOKINESIS DEFECTIVE 1, EMB101, EMBRYO DEFECTIVE 101, GDP-MANNOSE PYROPHOSPHORYLASE 1, GMP1, SOZ1, VITAMIN C DEFECTIVE 1, VTC1

Other Gene Models

name	description	source	date
CYT1	putative mannose-1-phosphate guanyltransferase	GenBank	1999-01-13
EMB101			
VTC1			
GMP1	GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds	GenBank	2002-10-16

Annotations

Category	Relationship Type	Keyword
GO Biological Process	involved in	cellulose biosynthesis
	none	biosynthesis
GO Cellular Component	located in	mitochondrion
GO Molecular Function	has activity	mannose-1-phosphate guanylyltransferase
	none	nucleotidyltransferase activity

Annotation Detail

RNA Data

Data from Expression Microarrays

array element name	alias(es)	avg. log ratio	std. error	expression viewer	SMD spot history
92D9	92D9T7	-0.018	0.028	Viewer	133665

Associated Transcripts

type	number associated
EST	(49)
cDNA	(5)

Description GDP-mannose pyrophosphorylase (GMP1), identical to GDP-mannose pyrophosphorylase from Arabidopsis thaliana (GI:3598958); updated per Conklin PL et al, PNAS 1999, 96 (7):4198-203

Chromosome 2

Nucleotide Sequence full length CDS full length genomic

Protein Data

name	Length (aa)	molecular weight	isoelectric point	domains(# of domains)
AT2G39770.1	361	39560.0	6.7194	G1P_thy_trans_I:IPR005907 (1) G1P_thy_trans_s:IPR005908 (1) Hexapep_transf:IPR001451 (4) ISPD:IPR001228(1)

Cons_hypoth454:IPR005245 (1)
GalF:IPR005774(1)
GalU:IPR005771(1)
GlmU:IPR005882(1)
NTP_transferase:IPR005835 (1)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
2	AGI	nuc_sequence	16595783 - 16598063 bp	forward	
2	T5I7	assembly_unit	31238 - 33518 bp	forward	details

Map Links Map Viewer Sequence Viewer

Gene Feature

type	coordinates	annotation source	date
ORF	697-2037	AGI-TIGR	2001-01-25
5' utr	1-133	AGI-TIGR	2001-01-25
5' utr	672-696	AGI-TIGR	2001-01-25
exon	1-133	AGI-TIGR	2001-01-25
intron	134-671	AGI-TIGR	2001-01-25
exon	672-807	AGI-TIGR	2001-01-25
intron	808-888	AGI-TIGR	2001-01-25
exon	889-951	AGI-TIGR	2001-01-25
intron	952-1039	AGI-TIGR	2001-01-25
exon	1040-1279	AGI-TIGR	2001-01-25
intron	1280-1365	AGI-TIGR	2001-01-25
exon	1366-2281	AGI-TIGR	2001-01-25
3' utr	2038-2281	AGI-TIGR	2001-01-25

Polymorphism

name	type
CYT1	unknown
SALK_049057.46.05.X	insertion
SALK_055122.43.70.X	insertion
SALK_082318.18.65.X	insertion
SALK_055115.53.30.X	insertion
SALK_038405	insertion
SALK_038406	insertion
SALK_048007.51.50.X	insertion
CYT1-1	insertion
CYT1-2	insertion
VTC1-1	unknown

External Link

MIPS View
TIGR View
View AraCyc information mannose and GDP-mannose metabolism
View AraCyc information colanic acid biosynthesis
View AraCyc information Reaction: 2.7.7.22
MPSS

AGI-TIGR's comment	updated per Conklin PL et al, PNAS 1999, 96(7):4198-203;supported by full-length cDNA: Ceres:37775.	2002-05-02

Comments (shows only the most recent comments by default)

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Attribution

type	name	date
submitted_by	David Meinke	2002-06-24
submitted_by	SSP Consortium: Salk, Stanford, PGEC	2002-06-24

Communication

Name	Author Name	associated gene models	date
Functional Genomic Characterization Effort	David Meinke		2002-06-24

Publication

title	source	associated gene models	date
Environmental stress sensitivity of an ascorbic acid-deficient Arabidopsis mutant.	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	VTC1	1996
L-ascorbic acid metabolism in the ascorbate-deficient arabidopsis mutant vtc1.	PLANT PHYSIOLOGY	VTC1	1997
A cytokinesis-defective mutant of Arabidopsis (cyt1) characterized by embryonic lethality, incomplete cell walls, and excessive callose accumulation.	THE PLANT JOURNAL	CYT1	1998
Genetic evidence for the role of GDP-mannose in plant ascorbic acid (vitamin C) biosynthesis.	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	VTC1	1999
Identification of ascorbic acid-deficient Arabidopsis thaliana mutants.	GENETICS	VTC1	2000
Transgenic overexpression of an ascorbic acid biosynthetic enzyme in Arabidopsis	11TH INTERNATIONAL CONFERENCE ON ARABIDOPSIS RESEARCH	VTC1	2000
Arabidopsis cyt1 mutants are deficient in a mannose-1-phosphate guanylyltransferase and point to a requirement of N-linked glycosylation for cellulose biosynthesis.	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	CYT1	2001